



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 29/674 19574

BEST AVAILABLE COPY

Source: PCT

Date Processed by STIC: 09/18/2001

BT AVAILABLE COPY

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/674 195A</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic <input type="checkbox"/> Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping".	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino <input type="checkbox"/> Numbering	The numbering under each 3 rd amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 <input type="checkbox"/> "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences <input type="checkbox"/> (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences <input type="checkbox"/> (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's <input type="checkbox"/> (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> <input type="checkbox"/> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input checked="" type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 <input type="checkbox"/> "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

AMC/MH - Biotechnology Systems Branch - 08/21/2001

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/674,195A

DATE: 09/18/2001
TIME: 13:30:00

Input Set : A:\14014.0325U2.TXT
Output Set: N:\CRF3\09182001\I674195A.raw

4 <110> APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, AS
5 REPRESENTED BY THE
6 SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
7 CENTERS FOR
8 DISEASE CONTROL AND PREVENTION
9 Rosely M. Zancope-Oliveira
10 Timothy J. Lott
11 Leonard W. Mayer
12 Errol Reiss
13 George S. Deepe

Does Not Comply
Corrected Diskette Needed

See Page 5 and 7

17 <120> TITLE OF INVENTION: NUCLEIC ACIDS OF THE M ANTIGEN GENE OF
18 HISTOPLASMA CAPSULATUM, ANTIGENS, VACCINES, AND ANTIBODIES,
19 METHODS AND KITS FOR DETECTING HISTOPLASMOsis

22 <130> FILE REFERENCE: 14114.0325U2
24 <140> CURRENT APPLICATION NUMBER: 09/674,195A
25 <141> CURRENT FILING DATE: 2000-10-26
27 <150> PRIOR APPLICATION NUMBER: 60/083,676
28 <151> PRIOR FILING DATE: 1998-04-30
30 <150> PRIOR APPLICATION NUMBER: PCT/US99/09151
31 <151> PRIOR FILING DATE: 1999-04-27
33 <160> NUMBER OF SEQ ID NOS: 13
35 <170> SOFTWARE: FastSEQ for Windows Version 4.0

37 <210> SEQ ID NO: 1

38 <211> LENGTH: 3862

39 <212> TYPE: DNA

40 <213> ORGANISM: Histoplasma capsulatum

42 <220> FEATURE:

43 <221> NAME/KEY: misc_feature

44 <222> LOCATION: (1)...(3862) ⑤

45 <223> OTHER INFORMATION: n = a,t,c, or g

47 <400> SEQUENCE: 1

48 ggatccgtcgata	ggctccgata	actttgcttt	atccaaagggt	ctcgccgaat	gccaggtgcc	60
49 atcgatctat	attttgaagt	ttatcaccc	aatggcttca	ccccatgacg	caccttttat	120
50 ttttattttc	attcatcttc	tctgtggcaa	acatgcagg	atgcgagctc	tggaccctgg	180
51 ggtgtggccc	ttgatgcata	tggtttattt	atagccgccc	ggaagccctg	gcctgttaaa	240
52 ttttggacct	cctcccgcca	ttctttccaa	acttcgtgcg	tccgtttccc	atttccccc	300
53 tccccatgg	ggttccctat	aggccactgc	gtgctccact	caagaagggt	cccagtcaat	360
54 ttggcccta	ccctctccaa	cactatctgc	atatgtaata	tatatcgata	tctaactgcc	420
55 attgattatt	tgtctcttc	agcatcttt	tgtctcgagc	aagcttactc	cacgttcaat	480
56 tcagggggta	aaaatgcgg	cgctcaagct	tatactcgcc	tccgtgggtg	ttgtttctgc	540
57 agcctgtccc	tacatgtcag	gggagatgcc	tagcgggtcag	aaaggcccc	tcgatcgccg	600
58 ccatgacact	ctctccgacc	ctacggacca	gtttcttagc	aagttttaca	ttgacgatga	660
59 acagtcgggt	ctaaacaacgg	acgtgggtgg	tcccatcgag	gaccaacaca	gcctgaaggc	720
60 tggaaataga	ggcccaactc	tacttgagga	ttttatcttc	cggcagaaga	ttcaacactt	780
61 tgatcatgag	agggtatgta	gataaaaaat	atgtgaccgt	gttgc当地atc	cgctaaattca	840
62 attttacgca	ggttcctgag	cgcgcgtcc	atgctcgagg	agctggtgcc	catggcgtat	900
63 tcacatccta	taataactgg	tcgaatataca	cagccgcatac	tttcttgaac	gcggcaggaa	960

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Input Set : A:\14014.0325U2.TXT
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64	agcagacacc	agtattcg	cggtttcta	cagtcgctgg	tagcagaggc	agtgttgact	1020							
65	ctgctcg	ga	tatccacgg	tttgcgaccc	gtctgtatac	cgatgaaggc	1080							
66	agcattat	at	cgtggtagtc	atactcataa	cagcacaaca	aatatgaata	1140							
67	acctagg	ctg	actactcg	gc	aatgttagata	tcgtcgaaa	1200							
68	ttcaggac	gc	tattcaattc	cctgatttga	ttcacgctgt	caagccgcaa	1260							
69	aaattcc	ca	ggctg	caact	gcacatgata	cggcatgg	1320							
70	gctcatt	gca	tgccctt	tggcaatgt	caggacatgg	aatccctcg	1380							
71	atgtt	gatgg	gtggggcg	tc	catac	ttcc	1440							
72	tgtcaag	tt	tcgctg	gaag	acccttca	gaagagcgg	1500							
73	ag	ctt	cg	ggaa	agaat	cccgactt	atcgaca	1560						
74	ctg	gaagg	ta	ccctg	gagtgg	gaggt	atgat	1620						
75	tgtt	ctct	ct	ctgtcg	tgctt	tttct	atatctt	caa	cta	1680				
76	ctt	tatata	ac	gttt	tactca	tatagctgg	cttcaattt	gt	gaatga	1740				
77	caag	ttt	gtat	ttcgat	ctat	tagatcccac	caa	atc	atc	ccaga	1800			
78	cac	ccca	atc	ggaaaat	tctg	aaacc	acc	aa	agttat	tttgc	1860			
79	gcag	atc	at	gttgg	tcc	ccct	tatata	ttt	gaat	atc	atgt	1920		
80	gaag	cg	tata	tctaa	atata	tttcc	acagt	tcc	acc	agg	tcatgt	1980		
81	attt	cac	gg	tgac	ccctt	tttgc	tttgc	gtt	act	ctac	cttgc	2040		
82	atcg	ccat	gg	agg	ccca	ac	tgc	gac	aa	tc	atcc	attcc	2100	
83	ataaca	aca	aa	tcg	cgac	gg	gttgg	ta	agc	t	ctt	tcac	2160	
84	ttgac	ccaa	at	cgat	ttt	gtt	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	2220	
85	cct	tctaa	ac	acgg	ccg	cat	at	ac	ac	cc	ac	ac	ac	2280
86	caac	ccgg	acc	cata	ac	ag	gat	ttc	tttgc	tttgc	tttgc	tttgc	tttgc	2340
87	agt	gcgc	gag	ctc	agcc	cc	gttca	ac	cg	tctgt	tttgc	tttgc	tttgc	2400
88	ctca	ctc	actc	ac	gtt	tc	act	cc	gt	ca	ac	gt	tttgc	2460
89	cgt	ccgg	gag	gaa	acc	gt	taa	gaa	ac	gt	cc	ac	cc	2520
90	cct	cgccc	gc	cg	gt	cc	cc	cc	cc	cc	cc	cc	cc	2580
91	ctacc	caca	ac	aagg	caacc	cc	ccc	atc	cc	cc	cc	cc	cc	2640
92	cg	gg	ctg	aaa	atc	cc	cct	cc	cc	cc	cc	cc	cc	2700
93	ccgg	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	2760
94	tgat	cccc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	2820
95	cgt	atcg	tc	ccgg	cc	cc	cc	cc	cc	cc	cc	cc	cc	2880
96	gtc	cagg	att	acgg	at	cc	cc	cc	cc	cc	cc	cc	cc	2940
97	tag	caat	gaa	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	3000
98	ggacc	agcc	cc	gg	ttt	cc	aa	cc	cc	cc	cc	cc	cc	3060
99	ggac	ggatt	g	acgg	cc	cc	cc	cc	cc	cc	cc	cc	cc	3120
100	agg	ttt	gggg	cg	cc	cc	cc	cc	cc	cc	cc	cc	cc	3180
101	ctgtt	tttcc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	3240
W--> 102	gcc	gg	gt	tc	ag	ttc	an	ga	gg	tt	ga	ag	tttgc	3300
103	gt	ta	ct	at	a	at	ttt	ttt	ttt	ttt	ttt	ttt	ttt	3360
104	tct	ca	at	tc	at	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	3420
105	gag	aca	aa	at	gat	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	3480
106	tca	gat	at	tc	at	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	3540
107	tga	at	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	3600
108	tgtt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	3660
109	tga	ct	at	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	3720
110	at	ag	at	aa	cc	cc	cc	cc	cc	cc	cc	cc	cc	3780
111	ta	ca	ta	at	cc	cc	cc	cc	cc	cc	cc	cc	cc	3840
112	aca	ac	ac	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	3862

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/674,195A

DATE: 09/18/2001
TIME: 13:30:01

Input Set : A:\14014.0325U2.TXT
Output Set: N:\CRF3\09182001\I674195A.raw

114 <210> SEQ ID NO: 2
115 <211> LENGTH: 707
116 <212> TYPE: PRT
117 <213> ORGANISM: Histoplasma capsulatum
119 <400> SEQUENCE: 2
120 Met Pro Ser Gly Gln Lys Gly Pro Leu Asp Arg Arg His Asp Thr Leu
121 1 5 10 15
122 Ser Asp Pro Thr Asp Gln Phe Leu Ser Lys Phe Tyr Ile Asp Asp Glu
123 20 25 30
124 Gln Ser Val Leu Thr Thr Asp Val Gly Gly Pro Ile Glu Asp Gln His
125 35 40 45
126 Ser Leu Lys Ala Gly Asn Arg Gly Pro Thr Leu Leu Glu Asp Phe Ile
127 50 55 60
128 Phe Arg Gln Lys Ile Gln His Phe Asp His Glu Arg Val Pro Glu Arg
129 65 70 75 80
130 Ala Val His Ala Arg Gly Ala Gly Ala His Gly Val Phe Thr Ser Tyr
131 85 90 95
132 Asn Asn Trp Ser Asn Ile Thr Ala Ala Ser Phe Leu Asn Ala Ala Gly
133 100 105 110
134 Lys Gln Thr Pro Val Phe Val Arg Phe Ser Thr Val Ala Gly Ser Arg
135 115 120 125
136 Gly Ser Val Asp Ser Ala Arg Asp Ile His Gly Phe Ala Thr Arg Leu
137 130 135 140
138 Tyr Thr Asp Glu Gly Asn Phe Asp Ile Val Gly Asn Asn Val Pro Val
139 145 150 155 160
140 Phe Phe Ile Gln Asp Ala Ile Gln Phe Pro Asp Leu Ile His Ala Val
141 165 170 175
142 Lys Pro Gln Pro Asp Ser Glu Ile Pro Gln Ala Ala Thr Ala His Asp
143 180 185 190
144 Thr Ala Trp Asp Phe Leu Ser Gln Gln Pro Ser Ser Leu His Ala Leu
145 195 200 205
146 Phe Trp Ala Met Ser Gly His Gly Ile Pro Arg Ser Met Arg His Val
147 210 215 220
148 Asp Gly Trp Gly Val His Thr Phe Arg Leu Val Thr Asp Glu Gly Asn
149 225 230 235 240
150 Ser Thr Leu Val Lys Phe Arg Trp Lys Thr Leu Gln Gly Arg Ala Gly
151 245 250 255
152 Leu Val Trp Glu Glu Ala Gln Ala Leu Gly Gly Lys Asn Pro Asp Phe
153 260 265 270
154 His Arg Gln Asp Leu Trp Asp Ala Ile Glu Ser Gly Arg Tyr Pro Glu
155 275 280 285
156 Trp Glu Leu Gly Phe Gln Leu Val Asn Glu Ala Asp Gln Ser Lys Phe
157 290 295 300
158 Asp Phe Asp Leu Leu Asp Pro Thr Lys Ile Ile Pro Glu Glu Leu Val
159 305 310 315 320
160 Pro Phe Thr Pro Ile Gly Lys Met Val Leu Asn Arg Asn Pro Lys Ser
161 325 330 335
162 Tyr Phe Ala Glu Thr Glu Gln Ile Met Phe Gln Pro Gly His Val Val
163 340 345 350

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Input Set : A:\14014.0325U2.TXT
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164 Arg Gly Ile Asp Phe Thr Asp Asp Pro Leu Leu Gln Gly Arg Leu Tyr
 165 355 360 365
 166 Ser Tyr Leu Asp Thr Gln Leu Asn Arg His Gly Gly Pro Asn Phe Glu
 167 370 375 380
 168 Gln Leu Pro Ile Asn Arg Pro Arg Ile Pro Phe His Asn Asn Asn Arg
 169 385 390 395 400
 170 Asp Gly Ala Gly Gln Met Phe Ile Pro Leu Asn Thr Ala Ala Tyr Thr
 171 405 410 415
 172 Pro Asn Ser Met Ser Asn Gly Phe Pro Gln Gln Ala Asn Arg Thr His
 173 420 425 430
 174 Asn Arg Gly Phe Phe Thr Ala Pro Gly Arg Met Val Asn Gly Pro Leu
 175 435 440 445
 176 Val Arg Glu Leu Ser Pro Ser Phe Asn Asp Val Trp Ser Gln Pro Arg
 177 450 455 460
 178 Leu Phe Tyr Asn Ser Leu Thr Val Phe Glu Lys Gln Phe Leu Val Asn
 179 465 470 475 480
 180 Ala Met Arg Phe Glu Asn Ser His Val Arg Ser Glu Thr Val Arg Lys
 181 485 490 495
 182 Asn Val Ile Ile Gln Leu Asn Arg Val Asp Asn Asp Leu Ala Arg Arg
 183 500 505 510
 184 Val Ala Leu Ala Ile Gly Val Glu Pro Pro Ser Pro Asp Pro Thr Phe
 185 515 520 525
 186 Tyr His Asn Lys Ala Thr Val Pro Ile Gly Thr Phe Gly Thr Asn Leu
 187 530 535 540
 188 Leu Arg Leu Asp Gly Leu Lys Ile Ala Leu Leu Thr Arg Asp Asp Gly
 189 545 550 555 560
 190 Ser Phe Thr Ile Ala Glu Gln Leu Arg Ala Ala Phe Asn Ser Ala Asn
 191 565 570 575
 192 Asn Lys Val Asp Ile Val Leu Val Gly Ser Ser Leu Asp Pro Gln Arg
 193 580 585 590
 194 Gly Val Asn Met Thr Tyr Ser Gly Ala Asp Gly Ser Ile Phe Asp Ala
 195 595 600 605
 196 Val Ile Val Val Gly Gly Leu Leu Thr Ser Ala Ser Thr Gln Tyr Pro
 197 610 615 620
 198 Arg Gly Arg Pro Leu Arg Ile Ile Thr Asp Ala Tyr Ala Tyr Gly Lys
 199 625 630 635 640
 200 Pro Val Gly Ala Val Gly Asp Gly Ser Asn Glu Ala Leu Arg Asp Val
 201 645 650 655
 202 Leu Met Ala Ala Gly Gly Asp Ala Ser Asn Gly Leu Asp Gln Pro Gly
 203 660 665 670
 204 Val Tyr Ile Ser Asn Asp Val Ser Glu Ala Tyr Val Arg Ser Val Leu
 205 675 680 685
 206 Asp Gly Leu Thr Ala Tyr Arg Phe Leu Asn Arg Phe Pro Leu Asp Arg
 207 690 695 700
 208 Ser Leu Val
 209 705
 211 <210> SEQ ID NO: 3
 212 <211> LENGTH: 8
 213 <212> TYPE: PRT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/674,195A

DATE: 09/18/2001

TIME: 13:30:01

Input Set : A:\14014.0325U2.TXT

Output Set: N:\CRF3\09182001\I674195A.raw

214 <213> ORGANISM: *Histoplasma capsulatum*
 216 <400> SEQUENCE: 3
 217 Ser Asp Pro Thr Asp Gln Phe Leu
 218 1 5
 220 <210> SEQ ID NO: 4
 221 <211> LENGTH: 15
 222 <212> TYPE: PRT
 223 <213> ORGANISM: *Histoplasma capsulatum*
 225 <400> SEQUENCE: 4
 226 Asp Phe Ile Phe Arg Gln Lys Ile Gln His Phe Asp His Glu Arg
 227 1 5 10 15
 229 <210> SEQ ID NO: 5
 230 <211> LENGTH: 9
 231 <212> TYPE: PRT
 232 <213> ORGANISM: *Histoplasma capsulatum*
 234 <400> SEQUENCE: 5
 235 Thr Leu Gln Gly Arg Ala Gly Leu Val
 236 1 5
 238 <210> SEQ ID NO: 6
 239 <211> LENGTH: 16
 240 <212> TYPE: PRT
 241 <213> ORGANISM: *Histoplasma capsulatum*
 243 <400> SEQUENCE: 6
 244 Ala Gln Ala Leu Gly Gly Lys Asn Pro Asp Phe His Arg Gln Asp Leu
 245 1 5 10 15
 247 <210> SEQ ID NO: 7
 248 <211> LENGTH: 6
 249 <212> TYPE: PRT
 250 <213> ORGANISM: *Histoplasma capsulatum*
 252 <400> SEQUENCE: 7
 253 Ser Gly Arg Tyr Pro Glu
 254 1 5
 256 <210> SEQ ID NO: 8
 257 <211> LENGTH: 10
 258 <212> TYPE: PRT
 259 <213> ORGANISM: *Histoplasma capsulatum*
 261 <400> SEQUENCE: 8
 262 Phe Asp Phe Asp Leu Leu Asp Pro Thr Lys
 263 1 5 10
 265 <210> SEQ ID NO: 9
 266 <211> LENGTH: 14
 267 <212> TYPE: PRT
 268 <213> ORGANISM: Unknown
 W--> 270 <220> FEATURE:
 W--> 270 <223> OTHER INFORMATION:
 270 <400> SEQUENCE: 9
 271 Ile Ile Pro Glu Glu Leu Val Pro Phe Thr Pro Ile Gly Lys
 272 1 5 10
 274 <210> SEQ ID NO: 10

A 213 response of Unknown Requires an
~~223~~ explanation or description in field

223.

The type of errors shown exist throughout
 the Sequence Listing. Please check subsequent
 sequences for similar errors.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/674,195A

DATE: 09/18/2001
TIME: 13:30:02

Input Set : A:\14014.0325U2.TXT
Output Set: N:\CRF3\09182001\I674195A.raw

L:102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:270 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:270 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:279 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:279 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:293 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:300 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:300 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:308 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:308 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: